

ENTERED



1635

RAW SEQUENCE LISTING

DATE: 05/22/2002

PATENT APPLICATION: US/09/600,358A

TIME: 13:23:40

Input Set : A:\92906-2 seq 08-03-02 v2.txt

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7 <130> FILE REFERENCE: 92906-2
9 <140> CURRENT APPLICATION NUMBER: US 09/600358A
10 <141> CURRENT FILING DATE: 2000-09-25
12 <150> PRIOR APPLICATION NUMBER: CA 2,220,853
13 <151> PRIOR FILING DATE: 1998-01-16
15 <160> NUMBER OF SEQ ID NOS: 7
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20 <211> LENGTH: 3058
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31 1 5
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34 Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser Lys Lys Ile Thr Lys
35 10 15 20
37 gag gag ttt gcc aat gaa ttt ctg aag ctg aaa agg caa tct acc aag 152
38 Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys Arg Gln Ser Thr Lys
39 25 30 35
41 tac aag gca gac aaa acc tat cct aca act gtg gct gag aat gcc aag 200
42 Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val Ala Glu Asn Ala Lys
43 40 45 50
45 aat atc aag aaa aac aga tat aag gat att ttg ccc tat gat tat agc 248
46 Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu Pro Tyr Asp Tyr Ser
47 55 60 65
49 cgg gta gaa cta tcc ctg ata acc tct gat gag gat tcc agc tac atc 296
50 Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu Asp Ser Ser Tyr Ile
51 70 75 80 85
53 aat gcc aac ttc att aag gga gtt tat gga ccc aag gct tat att gcc 344
54 Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro Lys Ala Tyr Ile Ala
55 90 95 100
57 acc cag ggt cct tta tct aca acc ctc ctg gac ttc tgg agg atg att 392
58 Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp Phe Trp Arg Met Ile
59 105 110 115
61 tgg gaa tat agt gtc ctt atc att gtt atg gca tgc atg gag tat gaa 440
62 Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala Cys Met Glu Tyr Glu

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70	Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys Glu Ala Glu Lys Arg			
71	150	155	160	165
74	aaa tct gat tat ata atc agg act cta aaa gtt aag ttc aat agt gaa	584		
75	Lys Ser Asp Tyr Ile Arg Thr Leu Lys Val Lys Phe Asn Ser Glu			
76	170	175	180	
78	act cga act atc tac cag ttt cat tac aag aat tgg cca gac cat gat	632		
79	Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn Trp Pro Asp His Asp			
80	185	190	195	
82	gta cct tca tct ata gac cct att ctt gag ctc atc tgg gat gta cgt	680		
83	Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu Ile Trp Asp Val Arg			
84	200	205	210	
86	tgt tac caa gag gat gac agt gtt ccc ata tgc att cac tgc agt gct	728		
87	Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys Ile His Cys Ser Ala			
88	215	220	225	
90	ggc tgt gga agg act ggt gtt att tgt gct att gtt gat tat aca tgg	776		
91	Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile Val Asp Tyr Thr Trp			
92	230	235	240	245
94	atg ttg cta aaa gat ggg ata att cct gag aac ttc agt gtt ttc agt	824		
95	Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe Ser Val Phe Ser			
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98	ttg atc cgg gaa atg cgg aca cag agg cct tca tta gtt caa acg cag	872		
99	Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu Val Gln Thr Gln			
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102	gaa caa tat gaa ctg gtc tac aat gct gta tta gaa cta ttt aag aga	920		
103	Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu Leu Phe Lys Arg			
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106	cag atg gat gtt atc aga gat aaa cat tct gga aca gag agt caa gca	968		
107	Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr Glu Ser Gln Ala			
108	295	300	305	
110	aag cat tgt att cct gag aaa aat cac act ctc caa gca gac tct tat	1016		
111	Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln Ala Asp Ser Tyr			
112	310	315	320	325
114	tct cct aat tta cca aaa agt acc aca aaa gca gca aaa atg atg aac	1064		
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116	330	335	340	
118	caa caa agg aca aaa atg gaa atc aaa gaa tct tct tcc ttt gac ttt	1112		
119	Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser Ser Phe Asp Phe			
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122	agg act tct gaa ata agt gca aaa gaa gag cta gtt ttg cac cct gct	1160		
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126	aaa tca agc act tct ttt gac ttt ctg gag cta aat tac agt ttt gac	1208		
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132	390						395					400				405	
134	gtt	ggg	gag	cct	ctt	cag	aag	cat	caa	agt	ttg	gat	ttg	ggc	tct	ctt	1304
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136					410					415					420		
139	ttg	ttt	gag	gga	tgt	tct	aat	tct	aaa	cct	gta	aat	gca	gca	gga	aga	1352
140	Leu	Phe	Glu	Gly	Cys	Ser	Asn	Ser	Lys	Pro	Val	Asn	Ala	Ala	Gly	Arg	
141				425					430						435		
143	tat	ttt	aat	tca	aag	gtg	cca	ata	aca	cgg	acc	aaa	tca	act	cct	ttt	1400
144	Tyr	Phe	Asn	Ser	Lys	Val	Pro	Ile	Thr	Arg	Thr	Lys	Ser	Thr	Pro	Phe	
145			440					445						450			
147	gaa	ttg	ata	cag	cag	aga	gaa	acc	aag	gag	gtg	gac	agc	aag	gaa	aac	1448
148	Glu	Leu	Ile	Gln	Gln	Arg	Glu	Thr	Lys	Glu	Val	Asp	Ser	Lys	Glu	Asn	
149		455				460						465					
151	ttt	tct	tat	ttg	gaa	tct	caa	cca	cat	gat	tct	tgt	ttt	gta	gag	atg	1496
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153	470					475					480					485	
155	cag	gct	caa	aaa	gta	atg	cat	gtt	tct	tca	gca	gaa	ctg	aat	tat	tca	1544
156	Gln	Ala	Gln	Lys	Val	Met	His	Val	Ser	Ser	Ala	Glu	Leu	Asn	Tyr	Ser	
157				490						495					500		
159	ctg	cca	tat	gac	tct	aaa	cac	caa	ata	cgt	aat	gcc	tct	aat	gta	aag	1592
160	Leu	Pro	Tyr	Asp	Ser	Lys	His	Gln	Ile	Arg	Asn	Ala	Ser	Asn	Val	Lys	
161				505					510					515			
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164	His	His	Asp	Ser	Ser	Ala	Leu	Gly	Val	Tyr	Ser	Tyr	Ile	Pro	Leu	Val	
165			520					525					530				
167	gaa	aat	cct	tat	ttt	tca	tca	tgg	cct	cca	agt	ggt	acc	agt	tct	aag	1688
168	Glu	Asn	Pro	Tyr	Phe	Ser	Ser	Trp	Pro	Pro	Ser	Gly	Thr	Ser	Ser	Lys	
169		535					540					545					
171	atg	tct	ctt	gat	tta	cct	gag	aag	caa	gat	gga	act	gtt	ttt	cct	tct	1736
172	Met	Ser	Leu	Asp	Leu	Pro	Glu	Lys	Gln	Asp	Gly	Thr	Val	Phe	Pro	Ser	
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175	tct	ctg	ttg	cca	aca	tcc	tct	aca	tcc	ctc	ttc	tct	tat	tac	aat	tca	1784
176	Ser	Leu	Leu	Pro	Thr	Ser	Ser	Thr	Ser	Leu	Phe	Ser	Tyr	Tyr	Asn	Ser	
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181				585					590						595		
183	aac	cag	gag	tca	gct	gta	cta	gca	act	gct	cca	agg	ata	gat	gat	gaa	1880
184	Asn	Gln	Glu	Ser	Ala	Val	Leu	Ala	Thr	Ala	Pro	Arg	Ile	Asp	Asp	Glu	
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187	atc	ccc	cct	cca	ctt	cct	gta	cgg	aca	cct	gaa	tca	ttt	att	gtg	gtt	1928
188	Ile	Pro	Pro	Pro	Leu	Pro	Val	Arg	Thr	Pro	Glu	Ser	Phe	Ile	Val	Val	
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200 Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg Pro Ser Lys Ser
201                               665                               670                               675
204 gta aaa ctc cga agt cct aaa tca gaa cta cat caa gat cgt tct tct 2120
205 Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His Gln Asp Arg Ser Ser
206                               680                               685                               690
208 ccc cca cct cct ctc cca gaa aga act cta gag tcc ttc ttt ctt gcc 2168
209 Pro Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala
210                               695                               700                               705
212 gat gaa gat tgt atg cag gcc caa tct ata gaa aca tat tct act agc 2216
213 Asp Glu Asp Cys Met Gln Ala Gln Ser Ile Glu Thr Tyr Ser Thr Ser
214 710                               715                               720                               725
216 tat cct gac acc atg gaa aat tca aca tct tca aaa cag aca ctg aag 2264
217 Tyr Pro Asp Thr Met Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Lys
218                               730                               735                               740
220 act cct gga aaa agt ttc aca agg agt aag agt ttg aaa att ttg cga 2312
221 Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Leu Arg
222                               745                               750                               755
224 aac atg aaa aag agt atc tgt aat tct tgc cca cca aac aag cct gca 2360
225 Asn Met Lys Lys Ser Ile Cys Asn Ser Cys Pro Pro Asn Lys Pro Ala
226                               760                               765                               770
228 gaa tct gtt cag tca aat aac tcc agc tca ttt ctg aat ttt ggt ttt 2408
229 Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe
230                               775                               780                               785
232 gca aac cgt ttt tca aaa ccc aaa gga cca agg aat cca cca cca act 2456
233 Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Pro Thr
234 790                               795                               800                               805
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247 tgccagttat ttttattttt ttttactttt ctacataaac ataaacttca aaagggtttgt 2805
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253 tatttttgcc taaatggagt ataccttgta aatcttccca aatgttgttg aaaactggaa 2985
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273 Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val
274          35          40          45
276 Ala Glu Asn Ala Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu
277          50          55          60
279 Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu
280          65          70          75          80
282 Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro
283          85          90          95
285 Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp
286          100          105          110
288 Phe Trp Arg Met Ile Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala
289          115          120          125
291 Cys Met Glu Tyr Glu Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala
292          130          135          140
294 Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys
295          145          150          155          160
297 Glu Ala Glu Lys Arg Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val
298          165          170          175
300 Lys Phe Asn Ser Glu Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn
301          180          185          190
303 Trp Pro Asp His Asp Val Pro Ser Ile Asp Pro Ile Leu Glu Leu
304          195          200          205
306 Ile Trp Asp Val Arg Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys
307          210          215          220
309 Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile
310          225          230          235          240
312 Val Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn
313          245          250          255
315 Phe Ser Val Phe Ser Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser
316          260          265          270
318 Leu Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu
319          275          280          285
321 Glu Leu Phe Lys Arg Gln Met Asp Val Ile Arg Asp Lys His Ser Gly
322          290          295          300
324 Thr Glu Ser Gln Ala Lys His Cys Ile Pro Glu Lys Asn His Thr Leu
325          305          310          315          320
327 Gln Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala
328          325          330          335
330 Ala Lys Met Met Asn Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser
331          340          345          350
334 Ser Ser Phe Asp Phe Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu
335          355          360          365
337 Val Leu His Pro Ala Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu
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Seq#:4; Line(s) 729,730,731,732,733,734,735,736,737,738,739,740,741,742,743
Seq#:4; Line(s) 744,745,746,747,748,749,750,751,752,753,754,755,756,757,758
Seq#:4; Line(s) 759,760,761,762
Seq#:5; Line(s) 763,764,765,766,767,768,769,770,771,772,773,774,775,776,777
Seq#:5; Line(s) 778,779,780,781,782,783,784,785,786,787,789,790,791,792,793
Seq#:5; Line(s) 794,795,796,797,798,799,800,801,802,803,804,805,806,807,808
Seq#:5; Line(s) 809,810,811,812,813,814,815,816,817,818,819,820,821,822,823
Seq#:5; Line(s) 824,825,826,827,828,829,830,831,832,833,834,835,836,837,838
Seq#:5; Line(s) 839,840,841,842,843,844,845,846,847,848,849,850,851,852,854
Seq#:5; Line(s) 855,856,857,858,859,860,861,862,863,864,865,866,867,868,869
Seq#:5; Line(s) 870,871,872,873,874,875,876,877,878,879,880,881,882,883,884
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Seq#:5; Line(s) 900,901,902,903,904,905,906,907,908,909,910,911,912,913,914
Seq#:5; Line(s) 915,916,917,919,920,921,922,923,924,925
Seq#:6; Line(s) 926,927,928,929,930,931,932,933,934,935,936
Seq#:7; Line(s) 937,938,939,940,941,942,943

VERIFICATION SUMMARY

DATE: 05/22/2002

PATENT APPLICATION: US/09/600,358A

TIME: 13:23:41

Input Set : A:\92906-2 seq 08-03-02 v2.txt

Output Set: N:\CRF3\05222002\I600358A.raw